CLAIMS

1. An enzyme preparation consisting essentially of an enzyme which has cellulytic activity and comprises a first amino acid sequence having the following sequence

Thr Arg Xaa Xaa Asp Cys Cys Xaa Xaa Xaa Cys Xaa Trp Xaa (SEQ ID NO: 79)
1 2 3 4 5 6 7 8 9 10 11 12 13 14

and a second amino acid sequence having the following sequence

Trp Cys Cys Xaa Cys (SEQ ID NO: 80)
1 2 3 4 5

wherein,

(a) the amino acid residue at position 3 of the first sequence is Trp, Tyr or Phe;

(b) the amino acid residue at position 4 of the first sequence is Trp, Tyr or Phe;

(c) the amino acid residue at position 8 of the first sequence is Arg, Lys or His; and

(d) the amino acid residues at positions 9, 10, 12 and 14 of the first sequence and at position 4 of the second sequence are independently any of the 20 naturally occurring amino acid residues, provided that, in the first amino acid sequence, (i) when the amino acid residue at position 12 is Ser, then the amino acid residue at position 14 is not Ser, and (ii) when the amino acid residue at position 12 is Gly, then the amino acid residue at position 14 is not Ala.

2. The enzyme preparation of claim 1, wherein the amino acid residue at position 9 of the first sequence is selected from the group consisting of proline, threonine, valine, alanine, leucine, isoleucine, phenylalanine, glycine, cysteine, asparagine, glutamine, tyrosine, serine, methionine and tryptophan, preferably from the group consisting of proline and threonine.

3. The enzyme preparation of claim 1, wherein the amino acid residue at position 10 of the first sequence is selected from the group consisting of proline, threonine, valine, alanine, leucine, isoleucine, phenylalanine, glycine, cysteine, asparagine, glutamine, tyrosine, serine, methionine and tryptophan, preferably serine.

4. The enzyme preparation of claim 1, wherein the amino acid residue at position 12 of the first sequence is selected from the group consisting of proline, threonine, valine, alanine, leucine, isoleucine, phenylalanine, glycine, cysteine, asparagine, glutamine, tyrosine, serine, methionine and tryptophan, preferably from the group consisting of alanine and glycine.

5. The enzyme preparation of claim 1, wherein the amino acid residue at position 14 of the first sequence is selected from the group consisting of proline, threonine, valine, alanine, leucine, isoleucine, phenylalanine, glycine, cysteine, asparagine, glutamine, tyrosine, serine, methionine, tryptophan, glutamic acid and aspartic acid, preferably from the group consisting of proline, threonine, serine, alanine, glutamic acid and aspartic acid.

6. The enzyme preparation of claim 1, wherein the amino acid residue at position 4 of the second sequence is selected from the group consisting of proline, threonine, valine, alanine, leucine, isoleucine, phenylalanine, glycine, cysteine, asparagine, glutamine, tyrosine, serine, methionine, tryptophan, glutamic acid and aspartic acid, preferably from the group consisting of alanine, glycine, and glutamine.

7. The enzyme preparation of claim 1, wherein, in the first sequence, the amino acid residue at position 3 is tyrosine; or the amino acid residue at position 4 is tryptophan; or the amino acid residue at position 8 is lysine.

8. The enzyme preparation of claim 1, wherein the first sequence comprises an amino acid sequence selected from the group consisting of the sequences

Thr Arg Tyr Trp Asp Cys Cys Lys Pro Ser Cys Ala Trp (SEQ ID NO: 79)
1 2 3 4 5 6 7 8 9 10 11 12 13;

Thr Arg Tyr Trp Asp Cys Cys Lys Thr Ser Cys Ala Trp (SEQ ID NO: 79)
1 2 3 4 5 6 7 8 9 10 11 12 13; and

Thr Arg Tyr Trp Asp Cys Cys Lys Pro Ser Cys Gly Trp (SEQ ID NO: 79)
1 2 3 4 5 6 7 8 9 10 11 12 13.

9. The enzyme preparation of claim 1 which is of microbial origin, preferably fungal origin.

10. A DNA construct encoding for the enzyme of claim 1.

11. An enzyme preparation consisting essentially of an enzyme having cellulytic activity and being obtainable from a strain belonging to Hymenomycetes (Basidiomycota) which enzyme comprises an amino acid sequence selected from the group consisting of the sequences

Xaa Thr Arg Xaa Phe Asp Xaa (SEQ ID NO: 105)
1 2 3 4 5 6 7;

Xaa Thr Arg Xaa Tyr Asp Xaa (SEQ ID NO: 106)
1 2 3 4 5 6 7; and
Xaa Thr Arg Xaa Trp Asp Xaa (SEQ ID NO: 107)
1 2 3 4 5 6 7

wherein,

(a) Xaa at position 4 is Trp, Tyr or Phe; and

(b) Xaa at positions 1 and 7 is independently any of the 20 naturally occurring amino acid residues.

12. The enzyme preparation of claim 11, wherein the amino acid residue at position 7 is cysteine.

13. The enzyme preparation of claim 11, wherein the amino acid residue at position 1 is selected from the group consisting of aspartic acid, threonine and alanine.

14. The enzyme preparation of claim 11, wherein the enzyme comprises a first peptide having the following sequence

Thr Arg Xaa Xaa Asp Cys Cys Xaa Xaa Xaa Cys Xaa Trp (SEQ ID NO: 79)
1 2 3 4 5 6 7 8 9 10 11 12 13

and a second peptide having the following sequence

Trp Cys Cys Xaa Cys (SEQ ID NO: 80)
1 2 3 4 5

wherein,

(a) the amino acid residue at position 3 of the first sequence is Trp, Tyr or Phe;

(b) the amino acid residue at position 4 of the first sequence is Trp, Tyr or Phe;

(c) the amino acid residue at position 8 of the first sequence is Arg, Lys or His;

(d) the amino acid residues at positions 9, 10, and 12 of the first sequence and at position 4 of the second sequence are independently any of the 20 naturally occurring amino acid residues.

15. The enzyme preparation of claim 11 wherein the enzyme is obtainable from a strain belonging to the group consisting of the orders *Agaricales*, *Aphyllophorales*, and *Auriculariales*.

16. The enzyme preparation of claim 15 wherein the enzyme is obtainable from a strain belonging to the group consisting of the families *Exidiaceae*, *Tricholomataceae*, *Coprinaceae*, *Schizophyllaceae*, *Bjerkanderaceae* and *Polyporaceae*, preferably belonging to the group consisting of the genera *Exidia*, *Crinipellis*, *Fomes*, *Panaeolus*, *Trametes*, *Schizophyllum*, and *Spongipellis*.

17. The enzyme preparation of claim 16 wherein the enzyme is obtainable from a strain belonging to the group consisting of the species *Exidia glandulosa*, *Crinipellis scabella*, *Fomes fomentarius*, and *Spongipellis sp.*, preferably from *Exidia glandulosa*, CBS 277.96, *Crinipellis scabella*, CBS 280.96, *Fomes fomentarius*, CBS 276.96, and *Spongipellis sp.*, CBS 283.96.

18. An enzyme preparation consisting essentially of an enzyme having cellulytic activity and being obtainable from a strain belonging to Chytridiomycota which enzyme comprises an amino acid sequence selected from the group consisting of the sequences

Xaa Thr Arg Xaa Phe Asp Xaa (SEQ ID NO: 105)
1 2 3 4 5 6 7;

Xaa Thr Arg Xaa Tyr Asp Xaa (SEQ ID NO: 106)
1 2 3 4 5 6 7; and

Xaa Thr Arg Xaa Trp Asp Xaa (SEQ ID NO: 107)
1 2 3 4 5 6 7

wherein,

Xaa at position 4 is Trp, Tyr or Phe; and

Xaa at positions 1 and 7 is independently any of the 20 naturally occurring amino acid residues.

19. The enzyme preparation of claim 18, wherein the amino acid residue at position 7 is cysteine.

20. The enzyme preparation of claim 18, wherein the amino acid residue at position 1 is selected from the group consisting of aspartic acid, threonine and alanine.

21. The enzyme preparation of claim 18, wherein the enzyme comprises a first peptide having the following sequence

Thr Arg Xaa Xaa Asp Cys Cys Xaa Xaa Xaa Cys Xaa Trp (SEQ ID NO: 79)
1 2 3 4 5 6 7 8 9 10 11 12 13

and a second peptide having the following sequence

Trp Cys Cys Xaa Cys (SEQ ID NO: 80)

1 2 3 4 5

wherein,

(a) the amino acid residue at position 3 of the first sequence is Trp, Tyr or Phe;

(b) the amino acid residue at position 4 of the first sequence is Trp, Tyr or Phe;

(c) the amino acid residue at position 8 of the first sequence is Arg, Lys or His; and

(d) the amino acid residues at positions 9, 10, and 12 of the first sequence, and at position 4 of the second sequence are independently any of the 20 naturally occurring amino acid residues.

22. The enzyme preparation of claim 18 wherein the enzyme is obtainable from a strain belonging to the class of *Chytridiomycetes*, preferably belonging to the group consisting of the orders *Chytridiales*, *Spizellomycetales*, *Harpochytriales*, and *Blastocladiales*.

23. The enzyme preparation of claim 22 wherein the enzyme is obtainable from a strain belonging the family *Spizellomycetaceae*, preferably belonging to the genus *Rhizophlyctis*, preferably belonging to the species *Rhizophlyctis rosea*, especially *R. rosea.*, CBS 282.96.

24. An enzyme preparation consisting essentially of an enzyme having cellulytic activity and being obtainable from a strain belonging to *Zygomycota* which enzyme comprises an amino acid sequence selected from the group consisting of the sequences

Xaa Thr Arg Xaa Phe Asp Xaa (SEQ ID NO: 105)

1 2 3 4 5 6 7;

Xaa Thr Arg Xaa Tyr Asp Xaa (SEQ ID NO: 106)

1 2 3 4 5 6 7; and

Xaa Thr Arg Xaa Trp Asp Xaa (SEQ ID NO: 107)

1 2 3 4 5 6 7

wherein,

(a) Xaa at position 4 is Trp, Tyr or Phe; and

(b) Xaa at positions 1 and 7 is independently any of the 20 naturally occurring amino acid residues.

25. The enzyme preparation of claim 24, wherein the amino acid residue at position 7 is cysteine.

26. The enzyme preparation of claim 24, wherein the amino acid residue at position 1 is selected from the group consisting of aspartic acid, threonine and alanine.

27. The enzyme preparation of claim 24, wherein the enzyme comprises a first peptide having the following sequence

Thr Arg Xaa Xaa Asp Cys Cys Xaa Xaa Xaa Cys Xaa Trp (SEQ ID NO: 108)
1 2 3 4 5 6 7 8 9 10 11 12 13

and a second peptide having the following sequence

Trp Cys Cys Xaa Cys (SEQ ID NO: 80)
1 2 3 4 5

wherein,

(a) the amino acid residue at position 3 of the first sequence is Trp, Tyr or Phe;

(b) the amino acid residue at position 4 of the first sequence is Trp, Tyr or Phe;

(c) the amino acid residue at position 8 of the first sequence is Arg, Lys or His;

(d) the amino acid residues at positions 9, 10, and 12 of the first sequence and at position 4 of the second sequence are independently any of the 20 naturally occurring amino acid residues.

28. The enzyme of claim 24 which enzyme is obtainable from a strain belonging to the class *Zygomycetes*, preferably to the order *Mucorales*.

29. The enzyme of claim 28 which enzyme is obtainable from a strain belonging to the group consisting of the families *Mucoracea* and *Thamnidiaceae*, preferably belonging to the group consisting of the genera *Rhizomucor*, *Phycomyces* and *Chaetostylum*.

30. The enzyme of claim 29 which enzyme is obtainable from a strain belonging the group consisting of the species *Rhizomucor pusillus*, *Phycomyces nitens*, *Chaetostylum fresenii*, preferably *Rhizomucor pusillus*, IFO 4578, *Phycomyces nitens*, IFO 4814, and *Chaetostylum fresenii*, NRRL 2305.

31. An enzyme preparation consisting essentially of an enzyme having cellulytic activity and being obtainable from a strain belonging to the group consisting of *Archaeascomycetes,*

Discomycetes, Hermiascomycetes, Loculoascomycetes, and Plectomycetes which enzyme comprises an amino acid sequence selected from the group consisting of the sequences

Xaa Thr Arg Xaa Phe Asp Xaa (SEQ ID NO: 105)
1 2 3 4 5 6 7;

Xaa Thr Arg Xaa Tyr Asp Xaa (SEQ ID NO: 106)
1 2 3 4 5 6 7; and

Xaa Thr Arg Xaa Trp Asp Xaa (SEQ ID NO: 107)
1 2 3 4 5 6 7

wherein,

(a) Xaa at position 4 is Trp, Tyr or Phe; and

(b) Xaa at positions 1 and 7 is independently any of the 20 naturally occurring amino acid residues.

32. The enzyme preparation of claim 31, wherein the amino acid residue at position 7 is cysteine.

33. The enzyme preparation of claim 31, wherein the amino acid residue at position 1 is selected from the group consisting of aspartic acid, threonine and alanine.

34. The enzyme preparation of claim 31, wherein the enzyme comprises a first peptide having the following sequence

Thr Arg Xaa Xaa Asp Cys Cys Xaa Xaa Xaa Cys Xaa Trp (SEQ ID NO: 108)
1 2 3 4 5 6 7 8 9 10 11 12 13

and a second peptide consisting of 5 amino acid residues having the following sequence

Trp Cys Cys Xaa Cys (SEQ ID NO: 80)
1 2 3 4 5

wherein,

(a) the amino acid residue at position 3 of the first sequence is Trp, Tyr or Phe;

(b) the amino acid residue at position 4 of the first sequence is Trp, Tyr or Phe;

(c) the amino acid residue at position 8 of the first sequence is Arg, Lys or His;

(d) the amino acid residues at positions 9, 10, and 12 of the first sequence and at position 4 of the second sequence are independently any of the 20 naturally occurring amino acid residues.

35. The enzyme preparation of claim 31 wherein the enzyme is obtainable from a strain belonging to the group consisting of the orders *Pezizales*, *Phytismatales*, *Dothideales*, and *Eurotiales*.

36. The enzyme preparation of claim 35 wherein the enzyme is obtainable from a strain belonging the the group consisting of the families *Cucurbitariaceae*, *Rhytismataceae*, *Ascobolaceae*, and *Trichocomaceae*, preferably belonging the the group consisting of the genera *Diplodia*, *Microsphaeropsis*, *Ulospora*, *Macrophomina*, *Ascobolus*, *Saccobolus*, *Penicillium*, and *Thermomyces*.

37. The enzyme preparation of claim 36 wherein the enzyme is obtainable from a strain belonging the the group consisting of the species *Diplodia gossypina*, *Microsphaeropsis sp.*, *Ulospora bilgramii*, *Macrophomina phaseolina*, *Ascobolus stictoides*, *Saccobolus dilutellus*, *Penicillium verruculosum*, *Penicillium chrysogenum*, and *Thermomyces verrucosus*, preferably *Diplodia gossypina*, CBS 274.96, *Ulospora bilgramii*, NKBC 1444, *Macrophomina phaseolina*, CBS 281.96, *Saccobolus dilutellus*, CBS 275.96, *Penicillium verruculosum*, ATCC 62396, *Penicillium chrysogenum*, ATCC 9480, and *Thermomyces verrucosus*, CBS 285.96.

38. An enzyme preparation consisting essentially of an enzyme having cellulytic activity and being obtainable from a strain belonging to the group consisting of the orders *Diaportales*, *Xylariales*, *Trichoaphaeriales* and *Phyllachorales* which enzyme comprises an amino acid sequence selected from the group consisting of the sequences

Xaa Thr Arg Xaa Phe Asp Xaa (SEQ ID NO: 105)
1 2 3 4 5 6 7;

Xaa Thr Arg Xaa Tyr Asp Xaa (SEQ ID NO: 106)
1 2 3 4 5 6 7; and

Xaa Thr Arg Xaa Trp Asp Xaa (SEQ ID NO: 107)
1 2 3 4 5 6 7

wherein,

(a) Xaa at position 4 is Trp, Tyr or Phe; and

(b) Xaa at positions 1 and 7 is independently any of the 20 naturally occurring amino acid residues.

39. The enzyme preparation of claim 38, wherein the amino acid residue at position 7 is cysteine.

40. The enzyme preparation of claim 38, wherein the amino acid residue at position 1 is selected from the group consisting of aspartic acid, threonine and alanine.

41. The enzyme preparation of claim 38, wherein the enzyme comprises a first peptide having the following sequence

Thr Arg Xaa Xaa Asp Cys Cys Xaa Xaa Xaa Cys Xaa Trp (SEQ ID NO: 108)
1 2 3 4 5 6 7 8 9 10 11 12 13

and a second peptide consisting of 5 amino acid residues having the following sequence

Trp Cys Cys Xaa Cys (SEQ ID NO: 80)
1 2 3 4 5

wherein,

(a) the amino acid residue at position 3 is Trp, Tyr or Phe;

(b) the amino acid residue at position 4 of the first sequence is Trp, Tyr or Phe;

(c) the amino acid residue at position 8 of the first sequence is Arg, Lys or His;

(d) the amino acid residues at positions 9, 10, and 12 of the first sequence and at position 4 of the second sequence are independently any of the 20 naturally occurring amino acid residues.

42. The enzyme preparation of claim 38 wherein the enzyme is obtainable from a strain belonging to the group consisting of the families *Xylariaceae*, *Valsaceae*, and *Phyllachoraceae*, preferably belonging to the genera *Diaporthe*, *Colletotrichum*, *Nigrospora*, *Xylaria*, *Nodulisporum* and *Poronia*.

43. The enzyme of claim 42 which enzyme is obtainable from a strain belonging to the group consisting of the species *Diaporthe syngenesia*, *Colletotrichum lagenarium*, *Nigrospora sp.*, *Xylaria hypoxylon*, *Nodulisporum sp.*, and *Poronia punctata*, preferably *Diaporthe syngenesia*, CBS 278.96, *Colletotrichum lagenarium*, ATCC 52609, *Nigrospora sp.*, CBS 272.96, *Xylaria hypoxylon*, CBS 284.96

44. An enzyme preparation consisting essentially of an enzyme having cellulytic activity and being obtainable from a strain belonging to the group consisting of the families *Nectriaceae*, *Sordariaceae*, *Chaetomiaceae*, *Ceratostomaceae*, *Lasiosphaeriaceae* and the genera *Acremonium*,

Gliocladium, *Scytalidium*, *Cylindrocarpon* and *Volutella* which enzyme comprises an amino acid sequence selected from the group consisting of the sequences

Xaa Thr Arg Xaa Phe Asp Xaa (SEQ ID NO: 105)
1 2 3 4 5 6 7;

Xaa Thr Arg Xaa Tyr Asp Xaa (SEQ ID NO: 106)
1 2 3 4 5 6 7; and

Xaa Thr Arg Xaa Trp Asp Xaa (SEQ ID NO: 107)
1 2 3 4 5 6 7

wherein,

(a) Xaa at position 4 is Trp, Tyr or Phe; and

(b) Xaa at positions 1 and 7 is independently any of the 20 naturally occurring amino acid residues.

45. The enzyme preparation of claim 44, wherein the amino acid residue at position 7 is cysteine.

46. The enzyme preparation of claim 44, wherein the amino acid residue at position 1 is selected from the group consisting of aspartic acid, threonine and alanine.

47. The enzyme preparation of claim 44, wherein the enzyme comprises a first peptide having the following sequence

Thr Arg Xaa Xaa Asp Cys Cys Xaa Xaa Xaa Cys Xaa Trp (SEQ ID NO: 79)
1 2 3 4 5 6 7 8 9 10 11 12 13

and a second peptide having the following sequence

Trp Cys Cys Xaa Cys (SEQ ID NO: 80)
1 2 3 4 5

wherein,

(a) the amino acid residue at position 3 of the first sequence is is Trp, Tyr or Phe;

(b) the amino acid residue at position 4 of the first sequence is Trp, Tyr or Phe;

(c) the amino acid residue at position 8 of the first sequence is Arg, Lys or His;

(d) the amino acid residues at positions 9, 10, and 12 of the first sequence and at position 4 of the second sequence are independently any of the 20 naturally occurring amino acid residues.

48. The enzyme preparation of claim 44, wherein the enzyme is obtainable from a strain belonging to the group consisting of the genera *Cylindrocarpon*, *Nectria*, *Volutella*, *Sordaria*, *Thielavia*, *Sypastospora*, *Chaetomium*, *Myceliophthora*, *Scytalidium*, *Cladorrhinum*, *Gliocladium*, *Acremonium*.

49. The enzyme of claim 48 which enzyme is obtainable from a strain belonging to the group consisting of the species *Cylindrocarpon sp.*, *Nectria pinea*, *Volutella colletotrichoides*, *Sordaria fimicola*, *Sordaria macrospora*, *Thielavia terrestris*, *Thielavia thermophila*, *Syspastospora boninensis*, *Cladorrhinum foecundissimum*, *Chaetomium murorum*, *Chaetomium virescens*, *Chaetomium brasiliensis*, *Chaetomium cunicolorum*, *Myceliophthora thermophila*, *Gliocladium catenulatum*, *Scytalidium thermophila*, and *Acremonium sp.*, preferably from *Gliocladium catenulatum*, ATCC 10523 & CBS 227.48, *Nectria pinea*, CBS 279.96, *Volutella colletotrichoides*, CBS 400.58, *Sordaria fimicola*, ATCC 52644, *Sordaria macrospora*, ATCC 60255, *Thielavia terrestris*, NRRL 8126, *Thielavia thermophila*, CCBS 174.70, *Chaetomium murorum*, CBS 163.52, *Chaetomium virescens*, CBS 547.75, *Chaetomium brasiliensis*, CBS 122.65, *Chaetomium cunicolorum*, CBS 799.83, *Syspastospora boninensis*, NKBC 1515, *Cladorrhinum foecundissimum*, ATCC 62373, *Myceliophthora thermophila*, CBS 117.65, *Scytalidium thermophila*, ATCC 28085, and *Acremonium sp.*, CBS 478.94.

50. An enzyme preparation consisting essentially of an enzyme having cellulytic activity and being obtainable from a strain belonging to the group consisting of the species *Fusarium lycopersici*, *Fusarium passiflora*, *Fusarium solani*, *Fusarium anguioides*, *Fusarium poae*, *Humicola nigrescens* and *Humicola grisea* which enzyme comprises an amino acid sequence selected from the group consisting of the sequences

Xaa Thr Arg Xaa Phe Asp Xaa (SEQ ID NO: 105)
1 2 3 4 5 6 7;
Xaa Thr Arg Xaa Tyr Asp Xaa (SEQ ID NO: 106)
1 2 3 4 5 6 7; and
Xaa Thr Arg Xaa Trp Asp Xaa (SEQ ID NO: 107)
1 2 3 4 5 6 7

wherein,

(a) Xaa at position 4 is Trp, Tyr or Phe; and

(b) Xaa at positions 1 and 7 is independently any of the 20 naturally occurring amino acid residues.

51. The enzyme preparation of claim 50, wherein the amino acid residue at position 7 is cysteine.

52. The enzyme preparation of claim 50, wherein the amino acid residue at position 1 is selected from the group consisting of aspartic acid, threonine and alanine.

53. The enzyme preparation of claim 50, wherein the enzyme comprises a first peptide having the following sequence

Thr Arg Xaa Xaa Asp Cys Cys Xaa Xaa Xaa Cys Xaa Trp (SEQ ID NO: 79)
1 2 3 4 5 6 7 8 9 10 11 12 13

and a second peptide having the following sequence

Trp Cys Cys Xaa Cys (SEQ ID NO: 80)
1 2 3 4 5

wherein,

(a) the amino acid residue at position 3 of the first sequence is Trp, Tyr or Phe;

(b) the amino acid residue at position 4 of the first sequence is Trp, Tyr or Phe;

(c) the amino acid residue at position 8 of the first sequence is Arg, Lys or His;

(d) the amino acid residues at positions 9, 10, and 12 of the first sequence and at position 4 of the second sequence are independently any of the 20 naturally occurring amino acid residues.

54. The enzyme preparation of claim 53, wherein the enzyme is obtainable from a strain belonging to the group consisting of the strains *Fusarium oxysporum ssp. lycopersici*, CBS 645.78, *Fusarium oxysporum ssp. passiflora*, CBS 744.79, *Fusarium solani*, IMI 107.511, *Fusarium anguioides*, IFO 4467, *Fusarium poae*, ATCC 60883, *Humicola nigrescens*, CBS 819.73 and *Humicola grisea*, ATCC 22726.

55. The enzyme preparation of claim 14, wherein the amino acid residue at position 9 of the first sequence is selected from the group consisting of proline, threonine, valine, alanine, leucine, isoleucine, phenylalanine, glycine, cysteine, asparagine, glutamine, tyrosine, serine, methionine and tryptophan, preferably from the group consisting of proline and threonine.

56. The enzyme of claim 14, wherein the amino acid residue at position 10 of the first sequence is selected from the group consisting of proline, threonine, valine, alanine, leucine, isoleucine,

phenylalanine, glycine, cysteine, asparagine, glutamine, tyrosine, serine, methionine and tryptophan, preferably serine.

57. The enzyme of claim 14, wherein the amino acid residue at position 12 of the first sequence is selected from the group consisting of proline, threonine, valine, alanine, leucine, isoleucine, phenylalanine, glycine, cysteine, asparagine, glutamine, tyrosine, serine, methionine and tryptophan, preferably from the group consisting of alanine and glycine.

58. The enzyme of claim 14, wherein the amino acid residue at position 4 of the second sequence is selected from the group consisting of proline, threonine, valine, alanine, leucine, isoleucine, phenylalanine, glycine, cysteine, asparagine, glutamine, tyrosine, serine, methionine, tryptophan, glutamic acid and aspartic acid, preferably from the group consisting of alanine, glycine, and glutamine.

59. The enzyme of claim 14, wherein, in the first sequence, the amino acid residue at position 3 is tyrosine; or the amino acid residue at position 4 is tryptophan; or the amino acid residue at position 8 is lysine.

60. A DNA construct encoding for the enzyme of claim 11.

61. The enzyme preparation of claim 14, wherein the first sequence comprises an amino acid sequence selected from the group consisting of the sequences

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Thr Arg Tyr Trp Asp Cys Cys Lys Pro Ser Cys Ala Trp (SEQ ID NO: 79)
1   2   3   4   5   6   7   8   9   10  11  12  13;
Thr Arg Tyr Trp Asp Cys Cys Lys Thr Ser Cys Ala Trp (SEQ ID NO: 79)
1   2   3   4   5   6   7   8   9   10  11  12  13; and
Thr Arg Tyr Trp Asp Cys Cys Lys Pro Ser Cys Gly Trp (SEQ ID NO: 79)
1   2   3   4   5   6   7   8   9   10  11  12  13.
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62. A method for providing a microbial strain comprising a gene encoding for the enzyme present in the enzyme preparation of claim 1, comprising hybridization, e.g. PCR amplification, under standard conditions with an oligonucleotide derived from any of the conserved regions illustrated in Fig.1.

63. The method of claims 62, wherein the oligonucleotide comprises a nucleotide sequence encoding at least a pentapeptide comprised in a peptide selected from the group consisting of

a.

Thr Arg Xaa Xaa Asp Cys Cys Xaa Xaa Xaa Cys Xaa Trp Xaa (SEQ ID NO: 79)

1 2 3 4 5 6 7 8 9 10 11 12 13 14

wherein

(a) the amino acid residue at position 3 or 4 is Trp, Tyr or Phe;

(b) the amino acid residue at position 8 is Arg, Lys or His;

(c) the amino acid residues at positions 9, 10, 12 and 14 are independently any of the 20 naturally occurring amino acid residues; and

b.

Trp Cys Cys Xaa Cys Tyr (SEQ ID NO: 81)

1 2 3 4 5 6

wherein the amino acid residue at position 4 is any of the 20 naturally occurring amino acid residues; and

c.

Xaa Pro Gly Gly Gly Xaa Gly Xaa Phe (SEQ ID NO: 82)

1 2 3 4 5 6 7 8 9

wherein

(a) the amino acid residue at position 1 is Met or Ile;

(b) the amino acid residues at positions 6 and 8 are independently Leu, Ile or Val; and

d.

Gly Cys Xaa Xaa Arg Xaa Asp Trp Xaa (SEQ ID NO: 83)

1 2 3 4 5 6 7 8 9

wherein

(a) the amino acid residue at position 3 is any of the 20 naturally occurring amino acid residues;

(b) the amino acid residues at positions 4 and 6 are independently Trp, Tyr or Phe; and

(c) the amino acid residue at position 9 being Phe or Met.

64. The method of claim 62, wherein the oligonucleotide comprises a nucleotide sequence complementary to the sequences of claim 63.

65. The method of claim 63, wherein the oligonucleotide corresponds to a PCR primer selected from the group consisting of the PCR primers

sense,

5'-CCCCAAGCTTACI$^{A}/_{C}$GITA$^{C}/_{T}$TGGGA$^{C}/_{T}$TG$^{C}/_{T}$TG$^{C}/_{T}$AA$^{A}/_{G}$$^{A}/_{C}$C-3' (SEQ ID NO: 84);

antisense 1,

5'- CTAGTCTAGATA$^{A}/_{G}$CAIGC$^{A}/_{G}$CA$^{A}/_{G}$CACC -3' (SEQ ID NO: 85);

antisense 2,

5'- CTAGTCTAGAAAIA$^{A}/_{G}$/^{T}ICCIA$^{A}/_{G}$/^{G}ICCICCICCIGG -3' (SEQ ID NO: 86); and

antisense 3,

5'- CTAGTCTAGAIAACCA$^{A}/_{G}$TCA$^{A}/_{G}$$^{A}/_{T}AIC^{G}/_{T}$CC -3 (SEQ ID NO: 87).

66. A DNA construct comprising a DNA sequence encoding an enzyme exhibiting cellulytic activity, which DNA sequence comprises

(a) the DNA sequence of SEQ ID NO: 1, and/or the DNA sequence obtainable from the plasmid in *Saccharomyces cerevisiae* DSM 9770, or

(b) an analogue of the DNA sequence of SEQ ID NO: 1 or the DNA sequence obtainable from the plasmid in *Saccharomyces cerevisiae* DSM 9770, which

(i) is homologous, preferably at least 70% homologous, with the DNA sequence of SEQ ID NO: 1 and/or the DNA sequence obtainable from the plasmid in *Saccharomyces cerevisiae* DSM 9770,

(ii) hybridizes under the conditions described herein with the same nucleotide probe as the DNA sequence of SEQ ID NO: 1 and/or the DNA sequence obtainable from the plasmid in *Saccharomyces cerevisiae* DSM 9770,

(iii) encodes a polypeptide which is homologous preferably at least 65% homologous, with the polypeptide encoded by a DNA sequence comprising the DNA sequence of SEQ ID NO: 1 and/or the DNA sequence obtainable from the plasmid in *Saccharomyces cerevisiae* DSM 9770,

(iv) encodes a polypeptide which is immunologically reactive with an antibody raised against the purified endoglucanase encoded by the DNA sequence of SEQ ID NO: 1 or obtainable from the plasmid in *Saccharomyces cerevisiae*, DSM 9770.

67. The DNA construct of claim 66, in which the DNA sequence is isolated from or produced on the basis of a DNA library of a strain belonging to the family *Chaetomiaceae*, preferably to the genus *Myceliophthora*, in particular a strain of *M. thermophila*, especially *M. thermophila*, CBS 117.65.

68. A DNA construct comprising a DNA sequence encoding an enzyme exhibiting endoglucanase activity, which DNA sequence comprises

(a) the DNA sequence of SEQ ID NO: 4, and/or the DNA sequence obtainable from the plasmid in *Saccharomyces cerevisiae* DSM 10082, or

(b) an analogue of the DNA sequence of SEQ ID NO: 4 or the DNA sequence obtainable from the plasmid in *Saccharomyces cerevisiae* DSM 10082, which

(i) is homologous, preferably at least 70% homologous, with the DNA sequence of SEQ ID NO: 4 and/or the DNA sequence obtainable from the plasmid in *Saccharomyces cerevisiae* DSM 10082,

(ii) hybridizes under the conditions described herein with the same nucleotide probe as the DNA sequence of SEQ ID NO: 4 and/or the DNA sequence obtainable from the plasmid in *Saccharomyces cerevisiae* DSM 10082,

(iii) encodes a polypeptide which is homologous preferably at least 60% homologous, with the polypeptide encoded by a DNA sequence comprising the DNA sequence of SEQ ID NO: and/or the DNA sequence obtainable from the plasmid in *Saccharomyces cerevisiae* DSM 10085,

(iv) encodes a polypeptide which is immunologically reactive with an antibody raised against the purified endoglucanase encoded by the DNA sequence of SEQ ID NO: 4 or obtainable from the plasmid in *Saccharomyces cerevisiae*, DSM 10082.

69. The DNA construct of claim 68, in which the DNA sequence is isolated from or produced on the basis of a DNA library of a strain belonging to the family *Hypocreaceae*, preferably to the genus *Acremonium*, in particular *Acremonium sp.*, CBS 478.94.

70. A DNA construct comprising a DNA sequence encoding an enzyme exhibiting endoglucanase activity, which DNA sequence comprises

(a) the DNA sequence of SEQ ID NO: 6, or the DNA sequence obtainable from the plasmid in *Saccharomyces cerevisiae* DSM 10080, or

(b) an analogue of the DNA sequence of SEQ ID NO: 6 or the DNA sequence obtainable from the plasmid in *Saccharomyces cerevisiae* DSM 10080, which

(i) is homologous, preferably 65% homologous, with the DNA sequence of SEQ ID NO: 6 or the DNA sequence obtainable from the plasmid in *Saccharomyces cerevisiae* DSM 10080,

(ii) hybridizes under the conditions described herein with the same nucleotide probe as the DNA sequence of SEQ ID NO: 6 or the DNA sequence obtainable from the plasmid in *Saccharomyces cerevisiae* DSM 10080,

(iii) encodes a polypeptide which is homologous, preferably at least 70%, with the polypeptide encoded by a DNA sequence comprising the DNA sequence of SEQ ID NO: 6 or the DNA sequence obtainable from the plasmid in *Saccharomyces cerevisiae* DSM 10080,

(iv) encodes a polypeptide which is immunologically reactive with an antibody raised against the purified endoglucanase encoded by the DNA sequence of SEQ ID NO: 6 /or obtainable from the plasmid in *Saccharomyces cerevisiae*, DSM 10080.

71. The DNA construct of claim 70, in which the DNA sequence is isolated from or produced on the basis of a DNA library of a strain belonging to the family *Chaetomiceae*, preferably to the genus *Acremonium*, in particular *Acremonium sp.*, CBS 478.94.

72. A DNA construct comprising a DNA sequence encoding an enzyme exhibiting endoglucanase activity, which DNA sequence comprises

(a) the DNA sequence of SEQ ID NO: 8, or the DNA sequence obtainable from the plasmid in *Saccharomyces cerevisiae* DSM 10081, or

(b) an analogue of the DNA sequence of SEQ ID NO: 8 or the DNA sequence obtainable from the plasmid in *Saccharomyces cerevisiae* DSM 10081, which

(i) is homologous, preferably at least 75% homologous, with the DNA sequence of SEQ ID NO: 8 or the DNA sequence obtainable from the plasmid in *Saccharomyces cerevisiae* DSM 10081,

(ii) hybridizes under the conditions described herein with the same nucleotide probe as the DNA sequence of SEQ ID NO: 8 or the DNA sequence obtainable from the plasmid in *Saccharomyces cerevisiae* DSM 10081,

(iii) encodes a polypeptide which is homologous, preferably at least 70% homologous, with the polypeptide encoded by a DNA sequence comprising the DNA sequence of SEQ ID NO: 8 or the DNA sequence obtainable from the plasmid in *Saccharomyces cerevisiae* DSM 10081,

(Iv) encodes a polypeptide which is immunologically reactive with an antibody raised against the purified endoglucanase encoded by the DNA sequence of SEQ ID NO: 8 or obtainable from the plasmid in *Saccharomyces cerevisiae*, DSM 10081.

73. The DNA construct of claim 72, in which the DNA sequence is isolated from or produced on the basis of a DNA library of a strain belonging to the family *Chaetomiaceae*, preferably to the genus *Thielavia*, in particular a strain of *Thielavia terrestris*, especially *Thielavia terrestris*, NRRL 8126.

74. A DNA construct comprising a DNA sequence encoding an enzyme exhibiting endoglucanase activity, which DNA sequence comprises

(a) the DNA sequence of SEQ ID NO: 10, or the DNA sequence obtainable from the plasmid in *Escherichia coli*, DSM 10512, or

(b) an analogue of the DNA sequence of SEQ ID NO: 10 or the DNA sequence obtainable from the plasmid in *Escherichia coli*, DSM 10512, which

(i) is homologous, preferably at least 65% homologous, with the DNA sequence of SEQ ID NO: 10 or the DNA sequence obtainable from the plasmid in *Escherichia coli*, DSM 10512,

(ii) hybridizes under the conditions described herein with the same nucleotide probe as the DNA sequence of SEQ ID NO: 10 or the DNA sequence obtainable from the plasmid in *Escherichia coli*, DSM 10512,

(iii) encodes a polypeptide which is homologous, preferably at least 55% homologous, with the polypeptide encoded by a DNA sequence comprising the DNA sequence of SEQ ID NO: 10 or the DNA sequence obtainable from the plasmid in *Escherichia coli*, DSM 10512,

(iv) encodes a polypeptide which is immunologically reactive with an antibody raised against the purified endoglucanase encoded by the DNA sequence of SEQ ID NO: 10 or obtainable from the plasmid in *Escherichia coli*, DSM 10512.

75. The DNA construct of claim 74, in which the DNA sequence is isolated from or produced on the basis of a DNA library of a strain belonging to the family *Rhytismataceae*, preferably to the genus *Macrophomina*, in particular *Macrophomina phaseolina*, especially *M. phaseolicola*, CBS 281.96.

76. A DNA construct comprising a DNA sequence encoding an enzyme exhibiting endoglucanase activity, which DNA sequence comprises

(a) the DNA sequence of SEQ ID NO: 12, or the DNA sequence obtainable from the plasmid in *Escherichia coli*, DSM 10511, or

(b) an analogue of the DNA sequence of SEQ ID NO: 12 or the DNA sequence obtainable from the plasmid in *Escherichia coli*, DSM 10511, which

(i) is homologous, preferably at least 60% homologous, with the DNA sequence of SEQ ID NO: 12 or the DNA sequence obtainable from the plasmid in *Escherichia coli*, DSM 10511,

(ii) hybridizes under the conditions described herein with the same nucleotide probe as the DNA sequence of SEQ ID NO: 12 or the DNA sequence obtainable from the plasmid in *Escherichia coli*, DSM 10511,

(iii) encodes a polypeptide which is homologous, preferably at least 60% homologous, with the polypeptide encoded by a DNA sequence comprising the DNA sequence of SEQ ID NO: 12 or the DNA sequence obtainable from the plasmid in *Escherichia coli*, DSM 10511,

(iv) encodes a polypeptide which is immunologically reactive with an antibody raised against the purified endoglucanase encoded by the DNA sequence of SEQ ID NO: 12 or obtainable from the plasmid in *Escherichia coli*, DSM 10511.

77. The DNA construct of claim 76, in which the DNA sequence is isolated from or produced on the basis of a DNA library of a strain belonging to the family Tricholomataceae, preferably to the genus *Crinipellis*, in particular *Crinipellis scabella*, especially *C. scabella*, CBS 280.96.

78. A DNA construct comprising a DNA sequence encoding an enzyme exhibiting endoglucanase activity, which DNA sequence comprises

(a) the DNA sequence of SEQ ID NO: 16, or the DNA sequence obtainable from the plasmid in *Escherichia coli*, DSM 10571, or

(b) an analogue of the DNA sequence of SEQ ID NO: 16 or the DNA sequence obtainable from the plasmid in *Escherichia coli*, DSM 10571, which

(i) is homologous, preferably at least 70 % homologous, with the DNA sequence of SEQ ID NO: 16 or the DNA sequence obtainable from the plasmid in *Escherichia coli*, DSM 10571,

(ii) hybridizes under the conditions described herein with the same nucleotide probe as the DNA sequence of SEQ ID NO: 16 or the DNA sequence obtainable from the plasmid in *Escherichia coli*, DSM 10571,

(iii) encodes a polypeptide which is homologous, preferably at least 60% hoologous, with the polypeptide encoded by a DNA sequence comprising the DNA

sequence of SEQ ID NO: 16 or the DNA sequence obtainable from the plasmid in *Escherichia coli*, DSM 10571,

(iv) encodes a polypeptide which is immunologically reactive with an antibody raised against the purified endoglucanase encoded by the DNA sequence of SEQ ID NO: 16 or obtainable from the plasmid in *Escherichia coli*, DSM 10571.

79. The DNA construct of claim 78, in which the DNA sequence is isolated from or produced on the basis of a DNA library of a strain of *Volutella*, in particular *Volutella colletotrichoides*, especially *V. colletotrochoides*, CBS 400.58.

80. A DNA construct comprising a DNA sequence encoding an enzyme exhibiting endoglucanase activity, which DNA sequence comprises

(a) the DNA sequence of SEQ ID NO: 19, or the DNA sequence obtainable from the plasmid in *Escherichia coli*, DSM 10576, or

(b) an analogue of the DNA sequence of SEQ ID NO: 19 or the DNA sequence obtainable from the plasmid in *Escherichia coli*, DSM 10576, which

(i) is homologous with the DNA sequence of SEQ ID NO: 19 or the DNA sequence obtainable from the plasmid in *Escherichia coli*, DSM 10576,

(ii) hybridizes under the conditions described herein with the same nucleotide probe as the DNA sequence of SEQ ID NO: 19 or the DNA sequence obtainable from the plasmid in *Escherichia coli*, DSM 10576,

(iii) encodes a polypeptide which is homologous with the polypeptide encoded by a DNA sequence comprising the DNA sequence of SEQ ID NO: 19 or the DNA sequence obtainable from the plasmid in *Escherichia coli*, DSM 10576,

(iv) encodes a polypeptide which is immunologically reactive with an antibody raised against the purified endoglucanase encoded by the DNA sequence of SEQ ID NO: 19 or obtainable from the plasmid in *Escherichia coli*, DSM 10576.

81. The DNA construct of claim 80, in which the DNA sequence is isolated from or produced on the basis of a DNA library of a strain belonging to the family of *Sordariaceae*, preferably to the genus *Sordaria*, in particular *Sordaria fimicola*, especially *S. fimicola*, ATCC 52644.

82. The DNA construct of claim 66 which further comprises a DNA sequence encoding a cellulose-binding domain.

83. The DNA construct of claim 82 which further comprises a DNA sequence encoding a cellulose-binding domain (CBD), the cellulose-binding domain and enzyme core (catalytically active domain) of the enzyme encoded by the DNA sequence of the DNA construct being operably linked.

84. A recombinant expression vector comprising a DNA construct of claim 66.

85. A cell comprising a DNA construct of claim 66.

86. A cell comprising a recombinant expression vector of claim 84.

87. A cell of claim 85, which is a eukaryotic cell, in particular a fungal cell, such as a yeast cell or a filamentous fungal cell, or an endogenous cell from which the gene originates.

88. A cell of claim 87, wherein the cell belongs to a strain of *Aspergillus*, *Fusarium*, or *Trichoderma*, in particular a strain of *Fusarium graminearum*, *Aspergillus niger* or *Aspergillus oryzae*.

89. A method of producing an enzyme exhibiting endoglucanase activity, comprising culturing a cell of claim 85 under conditions permitting the production of the enzyme, and recovering the enzyme from the culture.

90. An enzyme exhibiting endoglucanase activity, which enzyme

(a) is encoded by a DNA construct of claim 66,

(b) produced by the method of claim 88, or

(c) is immunologically reactive with an antibody raised against a purified endoglucanase encoded by the DNA sequence shown in any of the sequence listings SEQ ID NOS: 1, 4, 6, 8, 10, 12, 16, and 19.

91. A method of providing colour clarification of laundry, which method comprising treating the laundry with a soaking, washing or rinsing liquor comprising an enzyme preparation of claim 1.

92. The method of claim 91, wherein the laundry is treated in a washing machine.

93. The method of claim 91, wherein the endoglucanase is present in the soaking, washing, or rinsing liquor in an effective amount of between 1 and 1000 S-CEVU, preferably between 5 and 200 S-CEVU, per liter of liquor during machine cycle use conditions.

94. The method of claim 91, wherein the pH of the soaking, washing, or rinsing liquor is between 4 and 11, preferably between 6 and 10.5.

95. The method of claim 91, wherein the temperature is between 15□C and 60□C.

96. The method of claim 91, wherein the soaking, washing or rinsing liquor further comprises one or more enzymes selected from the group consisting of proteases, cellulases, xylanases, amylases, lipases, peroxidases and laccases.

97. A laundry composition comprising the enzyme preparation of claim 1, and a compound selected from the group consisting of a surfactant, a builder compound, and a fabric softening agent.

98. The laundry composition of claim 97, which further comprises one or more enzymes selected from the group consisting of proteases, amylases, lipases, cellulases, xylanases, peroxidases and laccases.

99. The composition of claim 97, wherein the surfactant is a nonionic, anionic, cationic, zwitterionic, ampholytic or amphoteric surfactant.

100. The composition of claim 97, wherein the fabric softening agent is a cationic or nonionic softening agent, preferably a quaternary ammonium compound, and which optionally further comprises one or more compounds selected from a surfactant, an electrolyte, a buffer, an antioxidant and a liquid carrier.

101. Use of the enzyme of claim 1 for degradation or modification of plant material, e.g. cell walls.

102. Use of the enzyme of claim 1 for treatment of fabric or textile, preferably for preventing backstaining, for bio-polishing or for "stone-washing" cellulosic fabric.

103. Use of the enzyme of claim 1 in the treatment of paper pulp, preferably for debarking, defibration, fibre modification, enzymatic de-inking or drainage improvement.

104. An enzyme preparation which is enriched in an enzyme exhibiting cellulytic activity of claim 1.

105. The preparation of claim 104, which additionally comprises one or more enzymes selected from the group consisting of galactanases, xylanases, arabinanases, pectin acetyl esterases, polygalacturonases, rhamnogalacturonases, pectin lyases, pectate lyases, endoglucanases, pectin methylesterases, proteases, lipases, amylases, cutinases, peroxidases, laccases, cellobiohydrolases and transglutaminases.